In the Specification.

Please amend the specification as follows deleting strikethrough text and adding underlined text:

Please amend the paragraph on page 12, beginning at line 6 through line 13 as follows:

--Sequence relationships between two or more nucleic acids or polynucleotides are generally defined as sequence identity, percentage of sequence identity. ~~See, for example, "Pedestrian Guide to Analyzing Sequence Data Bases" at www.embl-heidelberg.de/.about.schneide/paper/springer96/springer.html.~~ In determining sequence identity, a "reference sequence" is used as a basis for sequence comparison. The reference sequence may be a subset or the entirety of a specified sequence. That is, the reference sequence may be a full-length gene sequence or a segment of the gene sequence.--

Please amend the paragraph beginning on page 12, line 24, through page 13, line19 as follows:

--Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, Calif.); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG), 575 Science Drive, Madison, Wis., USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins et al. (1988) Gene 73:237-244; Higgins et al. (1989) CABIOS 5:151-153; Corpet et al. (1988) Nucleic Acids Res. 16:10881-90; Huang et al. (1992) CABIOS 8:155-65; and Pearson et al. (1994) Meth. Mol. Biol. 24:307-331. The ALIGN program is based on the algorithm of Myers and Miller (1988) supra. A

PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used with the ALIGN program when comparing amino acid sequences. The BLAST programs of Altschul et al (1990) J. Mol. Biol. 215:403 are based on the algorithm of Karlin and Altschul (1990) supra. BLAST nucleotide searches can be performed with the BLASTN program, score=100, wordlength=12, to obtain nucleotide sequences homologous to a nucleotide sequence encoding a protein of the invention. BLAST protein searches can be performed with the BLASTX program, score=50, wordlength=3, to obtain amino acid sequences homologous to a protein or polypeptide of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul et al. (1997) Nucleic Acids Res. 25:3389. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul et al. (1997) supra. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g., BLASTN for nucleotide sequences, BLASTX for proteins) can be used. ~~See http://www.ncbi.hlm.nih.- gov.~~ Alignment may also be performed manually by inspection.--

Please amend the paragraph on page 33, beginning at line 20 through line 31 as follows:

--In a first example of an miRNA precursor designed to target GUS, the backbone for the precursor is amplified by polymerase chain reaction (PCR) from ~~Arabidopsis thaliana~~ *Arabidopsis thaliana* genomic DNA using the sequence of the predicted precursor for an endogenous miRNA (miR167). The PCR product is isolated and cloned into the TA cloning vector. The cloned miRNA precursor backbone is further modified by standard cloning techniques to replace the miR167 sequence with the sequence "gcgtaagggt aatgcgaggt ac" (SEQ ID NO:1) which has complete complementarity to a 22 nucleotide region of nucleotides 9978-1000 within the GUS coding region. The entire GUS coding region is 1811 nucleotides. The endogenous

167miRNA sequence is located within the miRNA 167 precursor in a region that forms a double-stranded stem. Therefore, the designer GUS miRNA precursor will be further modified to recreate this region of double-strandedness (so that the GUS miRNA sequence will be located in a double-stranded stem in the precursor).--

Also enclosed herewith is a paper and computer readable copy of a sequence listing, containing all nucleotide sequences encompassed by the definitions for nucleotide and/or amino acid sequences as set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). Please amend the specification to add the sequence listing at the end of the specification.